

SEQUENCE LISTING



(1) GENERAL INFORMATION:

(i) APPLICANT: Gorman, Daniel M.  
Mattson, Jeanine D.

(ii) TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related Reagents  
X0510

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DNAX Research Institute  
(B) STREET: 901 California Avenue  
(C) CITY: Palo Alto  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94304-1104

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US  
(B) FILING DATE: 12-DEC-1997  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/032,846  
(B) FILING DATE: 13-DEC-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Ching, Edwin P.  
(B) REGISTRATION NUMBER: 34,090  
(C) REFERENCE/DOCKET NUMBER: DX0686

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (650) 852-9196  
(B) TELEFAX: (650) 496-1204

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2191 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 125..1072

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCCAGGACCT	CTGTGAACCG	GTCGGGGCGG	GGGCCGCCTG	GCCGGGAGTC	TGCTCGGC	60
TGGGTGGCCG	AGGAAGGGAG	AGAACCGATCG	CGGAGCAGGG	CGCCCGAACT	CCGGGCGCCG	120
CGCC ATG CGC CGG GCC AGC CGA GAC TAC GGC AAG TAC CTG CGC AGC TCG	Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser	1	5	10	15	169
GAG GAG ATG GCC AGC GGC CCC GGC GTC CCA CAC GAG GGT CCG CTG CAC	Glu Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His	20	25	30		217
CCC GCG CCT TCT GCA CCG GCT CCG GCG CCG CCA CCC GCC GCC TCC CGC	Pro Ala Pro Ser Ala Pro Ala Pro Pro Ala Ala Ser Arg	35	40	45		265
TCC ATG TTC CTG GCC CTC CTG GGG CTG GGA CTG GGC CAG GTG GTC TGC	Ser Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys	50	55	60		313
AGC ATC GCT CTG TTC CTG TAC TTT CGA GCG CAG ATG GAT CCT AAC AGA	Ser Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg	65	70	75		361
ATA TCA GAA GAC AGC ACT CAC TGC TTT TAT AGA ATC CTG AGA CTC CAT	Ile Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His	80	85	90	95	409
GAA AAC GCA GGT TTG CAG GAC TCG ACT CTG GAG AGT GAA GAC ACA CTA	Glu Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu	100	105	110		457
CCT GAC TCC TGC AGG AGG ATG AAA CAA GCC TTT CAG GGG GCC GTG CAG	Pro Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln	115	120	125		505
AAG GAA CTG CAA CAC ATT GTG GGG CCA CAG CGC TTC TCA GGA GCT CCA	Lys Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro	130	135	140		553
GCT ATG ATG GAA GGC TCA TGG TTG GAT GTG GCC CAG CGA GGC AAG CCT	Ala Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro	145	150	155		601
GAG GCC CAG CCA TTT GCA CAC CTC ACC ATC AAT GCT GCC AGC ATC CCA	Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro	160	165	170	175	649
TCG GGT TCC CAT AAA GTC ACT CTG TCC TCT TGG TAC CAC GAT CGA GGC	Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly	180	185	190		697

TGG GCC AAG ATC TCT AAC ATG ACG TTA AGC AAC GGA AAA CTA AGG GTT Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val 195 200 205	745
AAC CAA GAT GGC TTC TAT TAC CTG TAC GCC AAC ATT TGC TTT CGG CAT Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His 210 215 220	793
CAT GAA ACA TCG GGA AGC GTA CCT ACA GAC TAT CTT CAG CTG ATG GTG His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val 225 230 235	841
TAT GTC GTT AAA ACC AGC ATC AAA ATC CCA AGT TCT CAT AAC CTG ATG Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met 240 245 250 255	889
AAA GGA GGG AGC ACG AAA AAC TGG TCG GGC AAT TCT GAA TTC CAC TTT Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe 260 265 270	937
TAT TCC ATA AAT GTT GGG GGA TTT TTC AAG CTC CGA GCT GGT GAA GAA Tyr Ser Ile Asn Val Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu 275 280 285	985
ATT AGC ATT CAG GTG TCC AAC CCT TCC CTG CTG GAT CCG GAT CAA GAT Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp 290 295 300	1033
GCG ACG TAC TTT GGG GCT TTC AAA GTT CAG GAC ATA GAC TGAGACTCAT Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp 305 310 315	1082
TTCGTGAAAC ATTAGCATGG ATGTCCTAGA TGTGGAAA CTTCTTAAAA AATGGATGAT	1142
GTCTATACAT GTGTAAGACT ACTAAGAGAC ATGGCCCACG GTGTATGAAA CTCACAGCCC	1202
TCTCTCTTGA GCCTGTACAG GTTGTGTATA TGTAAAGTCC ATAGGTGATG TTAGATTCAT	1262
GGTGATTACA CAACGGTTTT ACAATTGT AATGATTCC TAAGAATTGA ACCAGATTGG	1322
GAGAGGTATT CCGATGCTTA TGAAAAACTT ACACGTGAGC TATGGAAGGG GGTCACAGTC	1382
TCTGGGTCTA ACCCCTGGAC ATGTGCCACT GAGAACCTTG AAATTAAGAA GATGCCATGT	1442
CATTGCAAAG AAATGATAGT GTGAAGGGTT AAGTTCTTT GAATTGTTAC ATTGCGCTGG	1502
GACCTGCAAA TAAGTTCTTT TTTCTAATG AGGAGAGAAA AATATATGTA TTTTTATATA	1562
ATGTCTAAAG TTATATTCA GGTGTAATGT TTTCTGTGCA AAGTTTGTA AATTATATTT	1622
GTGCTATAGT ATTGATTCA AAATATTTAA AAATGTCTCA CTGTTGACAT ATTAAATGTT	1682
TTAAATGTAC AGATGTATTT AACTGGTGCA CTTTGTAAATT CCCCTGAAGG TACTCGTAGC	1742
TAAGGGGGCA GAATACTGTT TCTGGTGACC ACATGTAGTT TATTCTTTA TTCTTTTAA	1802
CTTAATAGAG TCTTCAGACT TGTCAAAACT ATGCAAGCAA AATAAATAAA TAAAAATAAA	1862

ATGAATATCT	TGAATAATAA	GTAGGATGTT	GGTCACCAGG	TGCCTTCAA	ATTTAGAAGC	1922
TAATTGACTT	TAGGAGCTGA	CATAGCCAAA	AAGGATACAT	AATAGGCTAC	TGAAAATCTG	1982
TCAGGAGTAT	TTATGCAATT	ATTGAACAGG	TGTCTTTTT	TACAAGAGCT	ACAAATTGTA	2042
AATTTGTTT	CTTTTTTTTC	CCATAGAAAA	TGTACTATAG	TTTATCAGCC	AAAAAACAAAT	2102
CCACTTTTA	ATTTAGTGA	AGTTATTTTA	TTATACTGTA	CAATAAAAGC	ATTGTTCTG	2162
AATGGCATT	TTTGGTACTT	AAAAATGGC				2191

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Arg	Arg	Ala	Ser	Arg	Asp	Tyr	Gly	Lys	Tyr	Leu	Arg	Ser	Ser	Glu
1									10						15

Glu	Met	Gly	Ser	Gly	Pro	Gly	Val	Pro	His	Glu	Gly	Pro	Leu	His	Pro
									25						30

Ala	Pro	Ser	Ala	Pro	Ala	Pro	Ala	Pro	Pro	Ala	Ala	Ser	Arg	Ser
												35		40

Met	Phe	Leu	Ala	Leu	Leu	Gly	Leu	Gly	Leu	Gly	Gln	Val	Val	Cys	Ser
											50			55	60

Ile	Ala	Leu	Phe	Leu	Tyr	Phe	Arg	Ala	Gln	Met	Asp	Pro	Asn	Arg	Ile
										65				70	75

Ser	Glu	Asp	Ser	Thr	His	Cys	Phe	Tyr	Arg	Ile	Leu	Arg	Leu	His	Glu
										85				90	95

Asn	Ala	Gly	Leu	Gln	Asp	Ser	Thr	Leu	Glu	Ser	Glu	Asp	Thr	Leu	Pro
										100				105	110

Asp	Ser	Cys	Arg	Arg	Met	Lys	Gln	Ala	Phe	Gln	Gly	Ala	Val	Gln	Lys
										115				120	125

Glu	Leu	Gln	His	Ile	Val	Gly	Pro	Gln	Arg	Phe	Ser	Gly	Ala	Pro	Ala
										130				135	140

Met	Met	Glu	Gly	Ser	Trp	Leu	Asp	Val	Ala	Gln	Arg	Gly	Lys	Pro	Glu
										145				150	155

Ala	Gln	Pro	Phe	Ala	His	Leu	Thr	Ile	Asn	Ala	Ala	Ser	Ile	Pro	Ser
										165				170	175

Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp

180 185 190

Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn  
195 200 205

Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His  
210 215 220

Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr  
225 230 235 240

Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys  
245 250 255

Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr  
260 265 270

Ser Ile Asn Val Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile  
275 280 285

Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala  
290 295 300

Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp  
305 310 315

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**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s)



- 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- 7. Other: \_\_\_\_\_

**Applicant Must Provide:**

- An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-1123

For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-0400

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